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CUBN Is a Gene Locus for Albuminuria

Carsten A. Böger,¹ Ming-Huei Chen,² Adrienne Tin,³ Matthias Olden,^{1,4} Anna Köttgen,^{3,5} Ian H. de Boer,⁶ Christian Fuchsberger,⁷ Conall M. O'Seaghdha,⁸ Cristian Pattaro,⁷ Alexander Teumer,⁹ Ching-Ti Liu,¹⁰ Nicole L. Glazer,¹¹ Man Li,³ Jeffrey R. O'Connell,¹² Toshiko Tanaka,^{13,14} Carmen A. Peralta,¹⁵ Zoltán Kutalik,^{16,17} Jian'an Luan,¹⁸ Jing Hua Zhao,¹⁸ Shih-Jen Hwang,¹⁹ Erneg Akylbekova,²⁰ Holly Kramer,²¹ Pim van der Harst,²² Albert V. Smith,^{23,24} Kurt Lohman,²⁵ Mariza de Andrade,²⁶ Caroline Hayward,²⁷ Barbara Kollerits,²⁸ Anke Tönjes,²⁹ Thor Aspelund,^{23,24} Erik Ingelsson,³⁰ Gudny Eiriksdottir,²⁴ Lenore J. Launer,³¹ Tamara B. Harris,³¹ Alan R. Shuldiner,³² Braxton D. Mitchell,³³ Dan E. Arking,³⁴ Nora Franceschini,³⁵ Eric Boerwinkle,³⁶ Josephine Egan,³⁷ Dena Hernandez,³⁸ Muredach Reilly,³⁹ Raymond R. Townsend,⁴⁰ Thomas Lumley,¹¹ David S. Siscovick,⁴¹ Bruce M. Psaty,⁴² Bryan Kestenbaum,⁶ Talin Haritunians,⁴³ Sven Bergmann,^{16,17} Peter Vollenweider,⁴⁴ Gerard Waeber,⁴⁴ Vincent Mooser,⁴⁵ Dawn Waterworth,⁴⁵ Andrew D. Johnson,¹⁹ Jose C. Florez,⁴⁶ James B. Meigs,⁴⁷ Xiaoning Lu,¹⁰ Stephen T. Turner,⁴⁸ Elizabeth J. Atkinson,²⁶ Tennille S. Leak,⁴⁹ Knut Aasard,^{50,51} Frank Skorpen,⁵¹ Ann-Christine Syvänen,⁵² Thomas Illig,⁵³ Jens Baumert,⁵³ Wolfgang Koenig,⁵⁴ Bernhard K. Krämer,⁵⁵ Olivier Devuyst,⁵⁶ Josyf C. Mychaleckyj,⁵⁷ Cosetta Minelli,⁷ Stephan J.L. Bakker,⁵⁸ Lyudmyla Kedenko,⁵⁹ Bernhard Paulweber,⁵⁹ Stefan Coassin,²⁸ Karlhans Endlich,⁶⁰ Heyo K. Kroemer,⁶¹ Reiner Biffar,⁶² Sylvia Stracke,⁶³ Henry Völzke,⁶⁴ Michael Stumvoll,²⁹ Reedik Mägi,⁶⁵ Harry Campbell,⁶⁶ Veronique Vitart,²⁷ Nicholas D. Hastie,²⁷ Vilundur Gudnason,^{23,24} Sharon L.R. Kardia,⁶⁷ Yongmei Liu,²⁵ Ozren Polasek,⁶⁸ Gary Curhan,⁶⁹ Florian Kronenberg,²⁸ Inga Prokopenko,⁶⁵ Igor Rudan,⁷⁰ Johan Ärnlöv,⁷¹ Stein Hallan,^{50,51} Gerjan Navis,⁵⁸ the CKDGen Consortium, Afshin Parsa,⁷² Luigi Ferrucci,¹⁴ Josef Coresh,⁷³ Michael G. Shlipak,⁷⁴ Shelley B. Bull,⁷⁵ Andrew D. Paterson,⁷⁶ on behalf of DCCT/EDIC, H.-Erich Wichmann,^{53,77,78} Nicholas J. Wareham,¹⁸ Ruth J.F. Loos,¹⁸ Jerome I. Rotter,⁴³ Peter P. Pramstaller,⁷ L. Adrienne Cupples,¹⁰ Jacques S. Beckmann,⁷⁹ Qiong Yang,⁸⁰ Iris M. Heid,^{4,53} Rainer Rettig,⁸¹ Albert W. Dreisbach,⁸² Murielle Bochud,⁸³ Caroline S. Fox,^{19,84} and W.H.L. Kao⁸³

¹Department of Internal Medicine II, University Medical Center Regensburg, Regensburg, Germany;

²Department of Neurology, Boston University School of Medicine, Boston, Massachusetts;

³Department of Epidemiology and the Welch Center for Prevention, Epidemiology, and Clinical Research, Johns Hopkins University, Baltimore, Maryland;

⁴Department of Epidemiology and Preventive Medicine, Regensburg University Medical Center, Regensburg, Germany;

⁵Renal Division, University Hospital of Freiburg, Freiburg, Germany;

⁶Division of Nephrology, University of Washington, Seattle, Washington;

⁷Institute of Genetic Medicine, European Academy of Bolzano/Bozen (EURAC), Italy and Affiliated Institute of the University of Lübeck, Lübeck, Germany;

⁸Division of Nephrology, Brigham and Women's Hospital and Harvard Medical School, Boston Massachusetts;

⁹Interfaculty Institute for Genetics and Functional Genomics, University of Greifswald, Greifswald, Germany;

¹⁰Department of Biostatistics, Boston University School of Public Health and NHLBI's Framingham Heart Study, Boston Massachusetts;

¹¹Cardiovascular Health Research Unit and Department of Biostatistics, University of Washington, Seattle, Washington;

¹²University of Maryland School of Medicine, Baltimore, Maryland;

¹³Medstar Research Institute, Baltimore, Maryland;

¹⁴Clinical Research Branch, National Institute on Aging, Baltimore, Maryland;

¹⁵Division of Nephrology, University of California, San Francisco Medical School and San Francisco VA Medical Center, San Francisco, California;

¹⁶Department of Medical Genetics, University of Lausanne, Lausanne, Switzerland;

¹⁷Swiss Institute of Bioinformatics, Lausanne, Switzerland;

- 18 MRC Epidemiology Unit, Institute of Metabolic Science, Addenbrooke's Hospital, Cambridge, United Kingdom;
- 19 NHLBI's Framingham Heart Study and the Center for Population Studies, Framingham, Massachusetts;
- 20 Jackson State University, Jackson, Mississippi;
- 21 Loyola University, Maywood, Illinois;
- 22 Department of Cardiology, University Medical Center Groningen, University of Groningen, Groningen, The Netherlands;
- 23 University of Iceland, Reykjavik, Iceland;
- 24 Icelandic Heart Association, Hjartavernd, Holtasmara, Kopavogur, Iceland;
- 25 Department of Biostatistical Sciences, Wake Forest University, Division of Public Health Sciences, Winston-Salem, North Carolina;
- 26 Division of Biomedical Statistics and Informatics, Mayo Clinic, Rochester, Minnesota;
- 27 MRC Human Genetics Unit, Institute of Genetics and Molecular Medicine, Western General Hospital, Crewe Road, Edinburgh, Scotland;
- 28 Innsbruck Medical University, Division of Genetic Epidemiology, Innsbruck, Austria;
- 29 Department of Medicine, University of Leipzig, Leipzig, Germany;
- 30 Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, Sweden;
- 31 Laboratory of Epidemiology, Demography, and Biometry, NIA, Bethesda, Maryland;
- 32 University of Maryland School of Medicine, Geriatric Research and Education Clinical Center, Veterans Administration Medical Center, Baltimore, Maryland;
- 33 University of Maryland School of Medicine, Baltimore, Maryland;
- 34 McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins Medical Institutions, Baltimore, Maryland;
- 35 University of North Carolina at Chapel Hill, Chapel Hill, North Carolina;
- 36 Human Genetics Center, University of Texas Health Science Center, Houston, Texas;
- 37 Laboratory of Clinical Investigation, National Institute on Aging, Baltimore, Maryland;
- 38 Laboratory of Neurogenetics, National Institute on Aging, Bethesda, Maryland;
- 39 University of Pennsylvania Division of Cardiology, Perelman Center for Advanced Medicine, Philadelphia, Pennsylvania;
- 40 University of Pennsylvania Renal Electrolyte and Hypertension Division, Philadelphia, Pennsylvania;
- 41 Departments of Epidemiology and Medicine, University of Washington, Seattle, Washington;
- 42 Cardiovascular Health Research Unit, Departments of Medicine, Epidemiology, and Health Services and Group Health Research Institute, Group Health Cooperative, Seattle, Washington;
- 43 Medical Genetics Institute, Cedars-Sinai Medical Center, Los Angeles, California;
- 44 Department of Internal Medicine, Centre Hospitalier Universitaire Vaudois, Lausanne, Switzerland;
- 45 Genetics Division, GlaxoSmithKline, King of Prussia, Pennsylvania;
- 46 Center for Human Genetic Research and Diabetes Research Center (Diabetes Unit), Massachusetts General Hospital, Boston, Massachusetts, Program in Medical and Population Genetics, Broad Institute, Cambridge, Massachusetts, and Department of Medicine, Harvard Medical School, Boston, Massachusetts;
- 47 Department of General Internal Medicine, Massachusetts General Hospital, Boston, Massachusetts;
- 48 Department of Internal Medicine, Division of Nephrology and Hypertension, Mayo Clinic, Rochester, Minnesota;
- 49 Department of Epidemiology, Graduate School of Public Health, University of Pittsburgh, Pittsburgh, Pennsylvania;
- 50 St Olav University Hospital, Trondheim, Norway;
- 51 Faculty of Medicine, Norwegian University of Science and Technology (NTNU), Trondheim, Norway;
- 52 Molecular Medicine, Department of Medical Sciences, Science for Life Laboratory, Uppsala University, Uppsala, Sweden;
- 53 Institute of Epidemiology, Helmholtz Zentrum München, German Research Center for Environmental Health, Neuherberg, Germany;
- 54 Zentrum für Innere Medizin, Klinik für Innere Medizin II - Kardiologie, Universitätsklinikum Ulm, Ulm, Germany;
- 55 University Medical Centre Mannheim, 5th Department of Medicine, Mannheim, Germany;
- 56 NEFR Unit Université Catholique de Louvain Medical School, Brussels, Belgium;
- 57 Center for Public Health Genomics, Charlottesville, Virginia;
- 58 Department of Internal Medicine, University Medical Center, Groningen, University of Groningen, Groningen, The Netherlands;
- 59 First Department of Internal Medicine, Paracelsus Medical University, Salzburg, Austria;
- 60 Institute of Anatomy and Cell Biology, University of Greifswald, Greifswald, Germany;
- 61 Institute of Pharmacology, University of Greifswald, Greifswald, Germany;
- 62 Clinic for Prosthodontic Dentistry, Gerostomatology and Material Science, University of Greifswald, Greifswald, Germany;
- 63 Nephrology Clinic for Internal Medicine A, University of Greifswald, Greifswald, Germany;
- 64 Institute for Community Medicine, University of Greifswald, Greifswald, Germany;
- 65 Wellcome Trust Centre for Human Genetics, and Oxford Centre for Diabetes, Endocrinology and Metabolism, University of Oxford, United Kingdom;
- 66 Centre for Population Health Sciences, University of Edinburgh, Edinburgh, Scotland;
- 67

- University of Michigan School of Public Health, Department of Epidemiology, University of Michigan, Ann Arbor, Michigan;
 - ⁶⁸Gen-Info Ltd., Zagreb, Croatia;
 - ⁶⁹Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts;
 - ⁷⁰Center for Population Health Sciences, University of Edinburgh Medical School, Edinburgh, Scotland;
 - ⁷¹Department of Public Health and Caring Sciences, Uppsala University, Uppsala, Sweden;
 - ⁷²University of Maryland School of Medicine, Baltimore, Maryland;
 - ⁷³Welch Center for Prevention, Epidemiology & Clinical Research, Johns Hopkins University, Baltimore, Maryland;
 - ⁷⁴General Internal Medicine, University of California, San Francisco, San Francisco, California;
 - ⁷⁵Samuel Lunenfeld Research Institute of Mount Sinai Hospital, Prosserman Centre for Health Research, Toronto, Ontario, Canada;
 - ⁷⁶The Hospital for Sick Children, Toronto, Ontario, Canada;
 - ⁷⁷Institute of Medical Informatics, Biometry and Epidemiology, Ludwig-Maximilians-Universität, Munich, Germany;
 - ⁷⁸Klinikum Grosshadern, Munich, Germany;
 - ⁷⁹Service of Medical Genetics, Centre Hospitalier Universitaire Vaudois and University of Lausanne, Lausanne, Switzerland;
 - ⁸⁰Department of Biostatistics, Boston University School of Public Health, Boston, Massachusetts;
 - ⁸¹Institute of Physiology, University of Greifswald, Greifswald, Germany;
 - ⁸²University of Mississippi Division of Nephrology, University of Mississippi, Jackson, Mississippi;
 - ⁸³University Institute of Social and Preventive Medicine, Centre Hospitalier Universitaire Vaudois and University of Lausanne, IUMSP, Lausanne, Switzerland; and
 - ⁸⁴Division of Endocrinology, Brigham and Women's Hospital and Harvard Medical School, Boston, Massachusetts
- ✉ Corresponding author.

Correspondence: Caroline S. Fox, NHLBI's Framingham Heart Study, 73 Mount Wayte Avenue Suite #2, Framingham, MA 01702., Phone: 508-933-3477; Fax: 508-872-2678, E-mail: foxca@nhlbi.nih.gov; or W.H. Linda Kao, Departments of Epidemiology and Medicine, Johns Hopkins University, 615 N. Wolfe Street, Baltimore, MD 21205., Phone: 410-614-0945; Fax: 410-955-0863, E-mail: wkao@jhsp.edu. C.A.B., M.-H.C., A.T., M.O., A.K., and I.H.B. jointly contributed to this work. I.M.H., R.R., A.W.D., M.B., C.S.F., and W.H.L.K. jointly oversaw this work. C.A.B., M.-H.C., A.K., I.H.B., C.M.O., J.S.B., I.M.H., R.R., A.W.D., M.B., C.S.F., and W.H.L.K. comprise the writing group. A full list of members of the CKDGen Consortium is given in the Acknowledgments section.

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Abstract

Identification of genetic risk factors for albuminuria may alter strategies for early prevention of CKD progression, particularly among patients with diabetes. Little is known about the influence of common genetic variants on albuminuria in both general and diabetic populations. We performed a meta-analysis of data from 63,153 individuals of European ancestry with genotype information from genome-wide association studies (CKDGen Consortium) and from a large candidate gene study (CARE Consortium) to identify susceptibility loci for the quantitative trait urinary albumin-to-creatinine ratio (UACR) and the clinical diagnosis microalbuminuria. We identified an association between a missense variant (I2984V) in the *CUBN* gene, which encodes cubilin, and both UACR ($P = 1.1 \times 10^{-11}$) and microalbuminuria ($P = 0.001$). We observed similar associations among 6981 African Americans in the CARE Consortium. The associations between this variant and both UACR and microalbuminuria were significant in individuals of European ancestry regardless of diabetes status. Finally, this variant associated with a 41% increased risk for the development of persistent microalbuminuria during 20 years of follow-up among 1304 participants with type 1 diabetes in the prospective DCCT/EDIC Study. In summary, we identified a missense *CUBN* variant that associates with levels of albuminuria in both the general population and in individuals with diabetes.

Elevated levels of urinary albumin (albuminuria) are a cardinal manifestation of chronic kidney disease (CKD) and affect as many as 8% of adults from the United States¹ and 6% of adults from Germany.²

Higher levels of albuminuria, even within the low normal range, are associated with not only increased risks of ESRD but also cardiovascular disease and mortality.^{3–6} Moreover, the presence of albuminuria offers key prognostic information at each stage of decline in GFR.⁷ However, the pathophysiologic basis of albuminuria remains incompletely understood, and as a result, interventions for the prevention and treatment of albuminuria are limited.

Diabetes mellitus and hypertension are key risk factors for albuminuria, but neither of these factors fully account for the high prevalence of albuminuria nor its association with adverse health outcomes.⁸ Heritability of albuminuria ranges from 0.16 to 0.49 in families enriched with hypertension or diabetes.^{9,10} Rare genetic variants are known to cause monogenic diseases featuring severe, nephrotic range proteinuria.¹¹ However, linkage or candidate gene studies have not reproducibly identified common genetic variants in association with lower levels of albuminuria.^{9,10} Given recent successes in the use of genome-wide association studies (GWAS) of quantitative traits that can lead to the identification of relevant variants for a disease phenotype,^{12,13} we conducted a genome-wide association (GWA) analysis of albuminuria in 31,580 participants of European ancestry from the CKDGen Consortium, with follow-up in 27,746 additional participants. Albuminuria was analyzed as the quantitative trait urinary albumin-to-creatinine ratio (UACR) and as the dichotomous trait microalbuminuria (MA). Concurrently, we performed an analysis of albuminuria in the CARE Consortium using the ITMAT/Broad/CARE Vascular Disease 50k (IBC) single-nucleotide polymorphism (SNP) chip array¹⁴ in 19,499 Europeans and 6981 African Americans. Here, we report the results of our combined findings.

RESULTS

Study Samples

Basic characteristics of the participants from the studies in CKDGen and CARE are shown in [Table 1](#). Studies in these consortia are primarily population-based, with mean age ranging from 42 to 74 years. Details regarding study-specific genotyping information can be found in Supplemental Table 1, A and B, and in the Supplemental Text (Methods).

CKDGen Stage 1

[Figure 1A](#) and Supplemental Figure 1A show the Manhattan plots of the meta-analysis *P* values for UACR and microalbuminuria (UACR >25 mg/g [women], >17 mg/g [men]), respectively. Meta-analysis of GWAs from CKDGen stage 1 showed that no locus achieved genome-wide significance ($P < 5.0 \times 10^{-8}$) for either UACR or microalbuminuria in both the overall and the nondiabetic analyses. Supplemental Figure 2, A and B, shows the quantile-quantile plot of the UACR and microalbuminuria meta-analysis results.

CKDGen Stage 2 Follow-up

In CKDGen, the 16 top independent SNPs (*P* value range 1.1×10^{-7} to 5.7×10^{-6}) were moved into stage 2 follow-up in 15 additional studies ($n = 27,746$ individuals of European descent). These SNPs and their study-specific imputation scores are displayed in Supplemental Tables 2 and 3, respectively. Supplemental Table 4 shows the results of these 16 SNPs for all analyzed traits.

Overall, rs1801239, a missense SNP (T→C) located in *CUBN* on chromosome 10 (minor allele frequency = 0.10), demonstrated direction-consistent association in stage 2 ($P = 0.02$, [Table 2](#)), with a genome-wide significant *P* value of 4.0×10^{-8} for UACR in the combined stage 1 and stage 2 analysis

(Supplemental Tables 2 and 4). The regional association plot for *CUBN* is shown in Figure 2A. The minor C allele of rs1801239 in *CUBN* leads to an isoleucine-to-valine substitution (I2984V) in the encoded protein cubilin, which is predicted to be “probably benign” (SIFT,¹⁵ FastSNP,¹⁶ and PolyPhen¹⁷). No additional nonsynonymous coding variants in high LD to rs1801239 ($r^2 > 0.2$) were observed in dbSNP. Because albuminuria is a risk factor for progressive CKD, we assessed whether rs1801239 is associated with estimated GFR (eGFR) and CKD in the CKDGen eGFR data set. Among 67,093 individuals with available data, we observed no association with eGFR ($P = 0.53$) or CKD ($P = 0.33$).¹⁸

The second highest ranking SNP for UACR in the combined stage 1 and stage 2 analysis was rs17319721, an intronic SNP in *SHROOM3* (Supplemental Table 4). The minor allele (A) of rs17319721 is associated with lower albuminuria levels, and we have previously identified this same allele in association with lower eGFR.¹⁹

CARe IBC SNP Array Stage 1

Concurrently, the CARe Consortium carried out a large densely tagged candidate gene screen using the IBC SNP array¹⁴ and identified the same SNP (rs1801239) in *CUBN* in association with UACR ($P = 2.9 \times 10^{-10}$; Table 2 and Figure 1B) and microalbuminuria (2100 cases and $P = 2.4 \times 10^{-7}$; Table 2) in 19,499 European Americans. The regional association plot for the *CUBN* tagging SNPs on the IBC array in the CARe European Americans is shown in Figure 2B. The only other significant SNP (significance threshold defined as $P < 2.2 \times 10^{-6}$ for the IBC array) in the CARe IBC analysis for UACR was rs13177732 ($P = 4.7 \times 10^{-7}$), but this SNP did not replicate in CKDGen stage 1 (discovery) studies after excluding overlapping studies ($n = 16,667$, $P = 0.71$ for UACR).

Joint CKDGen/CARe Analyses in Samples of European Ancestry

Because three of the studies from CARe (ARIC, CHS, and FHS) were also part of CKDGen, we removed them from CKDGen to avoid duplication. The overall P value for CKDGen stage 1 (after removing ARIC, CHS, and FHS), CKDGen stage 2 follow-up (after removing the ARIC in silico replication samples), and the CARe stage 1 analysis in participants of European ancestry for the association between rs1801239 and UACR was 1.1×10^{-11} ($n = 63,153$; Table 2), with 0.15% of the UACR variance explained by rs1801239. The study-specific association results are shown in Supplemental Figure 3A; there was no significant heterogeneity across studies ($I^2 = 19.6\%$, P value for heterogeneity = 0.18). The odds ratio for microalbuminuria per copy of the minor C allele at rs1801239 was 1.06 ($P = 0.001$; Table 2).

CARe African-American IBC SNP Array Results

Because albuminuria is an important manifestation of CKD across ethnicities, we examined rs1801239 in 6981 African-American CARe participants (1159 microalbuminuria cases) and found that the minor C allele (frequency = 0.03) was consistently associated with higher UACR ($P = 0.005$, explaining 0.06% of the UACR variance) and the presence of microalbuminuria. Each copy of the C allele at rs1801239 was associated with an odds ratio of 1.42 for microalbuminuria ($P = 0.008$; Table 2). The study-specific association results for UACR are shown in Supplemental Figure 3B. Given the potential for allelic heterogeneity across ethnic groups and the availability of densely genotyped IBC chip data, we further investigated the *CUBN* region (Figure 2C) to determine if there were any other SNPs that showed stronger association with UACR and microalbuminuria in African Americans. We uncovered rs1996316 in the *CUBN* gene region (minor allele frequency = 0.33, P value = 0.0009). The SNP rs1996316 was not correlated with rs1801239 ($r^2 = 0.01$); however, this SNP did not meet statistical significance after

correcting for multiple testing of 158 SNPs in the region ($0.05/158 = 0.0003$), nor was it associated with UACR in individuals of European descent from CKDGen ($P = 0.65$) or CARE ($P = 0.36$).

Stratified Analysis

Because hypertension and diabetes are key risk factors for albuminuria, we performed stratified analyses for rs1801239 in the joint CKDGen/CARE analysis of populations of European descent. For UACR, we observed significant association among individuals with ($n = 4915$; $P = 0.006$) and without ($P = 3.2 \times 10^{-8}$) diabetes as well as among individuals with ($n = 13,097$, $P = 7.5 \times 10^{-8}$) and without ($P = 1.3 \times 10^{-6}$) hypertension. Similar findings across these groups were also observed for microalbuminuria (Table 2). In particular, among individuals with diabetes, each copy of the C allele at rs1801239 was associated with an odds ratio of 1.27 for microalbuminuria (95% CI: 1.11 to 1.45).

To investigate if CKD modifies the association between rs1801239 and UACR, we performed an analysis of rs1801239 and UACR in 6 of the largest cohorts in CKDGen stratified by CKD status. We found that the association of the *CUBN* C allele and UACR was of similar magnitude among participants with CKD ($n = 1808$, $\beta = 0.09$, $P = 0.26$) as compared with those without CKD ($n = 21299$, $\beta = 0.10$, $P = 9.6 \times 10^{-11}$), although the power was low in the CKD stratum because of its smaller sample size.

Independent Replication in the Diabetes Control and Complications Trial and Epidemiology of Diabetes Interventions and Complications (DCCT/EDIC)

To understand the potential impact of rs1801239 on microalbuminuria in a high-risk population, we tested the association of rs1801239 with time to persistent microalbuminuria over 20 years of follow-up among 1304 participants of European ancestry with type 1 diabetes from the DCCT/EDIC Study (mean baseline age 26.7 years). With use of survival analysis, the minor C allele was associated with an increased risk of incident persistent microalbuminuria. Individuals with diabetes with one copy of the C allele had a 42% greater risk of developing persistent microalbuminuria than their counterparts with zero copies of the C allele (hazard ratio 1.42 per copy of the C allele, $P = 0.02$; Table 2). This association was essentially unchanged with further multivariable adjustment (Table 2).

DISCUSSION

We have identified and validated a missense SNP in the *CUBN* gene that is associated with albuminuria. This association is robust across subgroups defined by diabetes and hypertension, two major risk factors for albuminuria, and among populations of both European and African ancestry. Finally, we have validated this finding in association with persistent microalbuminuria among patients with type 1 diabetes from the DCCT/EDIC Study.

Cubilin was first identified as the intrinsic factor/vitamin B12 complex receptor in the ileal mucosa.²⁰ In the kidney, cubilin is expressed predominantly in the apical brush border of proximal tubular cells.²¹ We queried publicly available expression databases^{22–24} but did not find evidence for altered gene expression associated with the conservative amino acid substitution in cubilin encoded by rs1801239 (I2984V). On the basis of UniProt, the amino acid position 2984 is part of the 22nd, out of a total of 27, CUB domains. *In vitro*, CUB domains 22 through 27 demonstrated Ca^{2+} -dependent binding to megalin.²⁵ Together with megalin (*LRP2*) and amnionless (*AMN*), cubilin plays a key role in the receptor-mediated endocytotic reabsorption of albumin and other low-molecular-weight proteins.²⁶ Interrogation of these respective genomic regions in our data did not reveal any significant findings. The process of endocytotic reabsorption of albumin is of importance because an estimated 3 g of albumin per day are not retained by the glomerular filter and enter the primary urine.²⁶ Yet urine in its

final composition is nearly devoid of proteins in healthy humans, highlighting the effectiveness of the tubular reabsorptive process to prevent significant protein loss.

The essential role of the cubilin-megalin complex in the reuptake of albumin by the proximal tubule has been demonstrated in both animal and human studies.^{26,27} For example, dogs with a functional defect in cubilin and mice lacking cubilin and/or megalin excrete large amounts of urinary albumin.^{27,28} Similarly, humans with Imerslund-Gräsbeck disease (OMIM #261100), a rare autosomal-recessive condition caused by a variety of mutations in the *CUBN* gene or the cubilin-associated *AMN* gene, typically have anemia with varying degrees of proteinuria²⁹ as a result of a molecular defect leading to inefficient proximal tubular protein reabsorption.

Dysfunction of the megalin-cubilin system has also been implicated in the pathogenesis of diabetic kidney disease. In rat models, renal tubular expression of cubilin is decreased³⁰ and reabsorption of filtered albumin by the proximal tubule has been shown to be altered.^{31,32} In humans, shedding of megalin and cubilin in urine is increased in individuals with type 1 diabetes and microalbuminuria compared with nonalbuminuric controls.³³ These studies suggest that reduced expression or loss of the cubilin-megalin complex may contribute to the albuminuria of early diabetic kidney disease via reduced tubular reuptake of filtered albumin, which is supported by our observed association of rs1801239 with incident persistent microalbuminuria in the DCCT/EDIC Study.

Our results suggest that levels of albuminuria in the general population are determined in part by tubular reabsorption, and not only by glomerular filtration. Although the prognostic implications of tubular as compared with glomerular albuminuria remain to be determined, a pathogenic role for tubular albuminuria, in addition to glomerular, has been demonstrated in experimental data.³⁴⁻³⁶ The identification of a SNP that is associated with albuminuria among individuals irrespective of diabetes or hypertension status suggests some common pathophysiology that is independent of these known albuminuria risk factors. The *CUBN* SNP we identified is specifically associated with albuminuria, and not with eGFR. Finally, results from the DCCT/EDIC Study underscore the relative strength of the *CUBN* SNP in association with persistent microalbuminuria that is comparable in magnitude to other albuminuria risk factors in patients with diabetes, including diabetes duration, BP, hemoglobin A1c, and obesity.³⁷⁻³⁹

Important strengths of this study include consistency of association across populations of European and African descent and across groups defined by diabetes and hypertension, as well as the known role of cubilin in tubular albumin reabsorption. The exploration of genetic determinants for albuminuria in predominantly population-based cohorts reduces confounding by disease progression, which may be related to important nongenetic factors. Nonetheless, some limitations warrant mention. First, the causal nature of the missense SNP in *CUBN* is unclear. Second, urine albumin and creatinine were assessed with different assays and at one point in time in most studies, which may lead to misclassification of the outcome and bias our results toward the null hypothesis. However, this is unlikely to yield a true positive finding.

In summary, through a series of genetic association analyses, we have identified a missense SNP in the *CUBN* gene that is associated with higher levels of albuminuria among individuals of European and African descent with and without diabetes or hypertension. These findings highlight a novel genetic susceptibility for albuminuria that is consistent across multiple study populations and shared across diverse clinical settings.

CONCISE METHODS

Overall Study Design

Genetic association testing for urinary albumin-to-creatinine ratio (UACR) and MA was performed in the CKDGen and CARE cohorts of European ancestry, with further follow-up genetic analysis of significant SNPs in CARE cohorts of African-American ancestry and in the Diabetes Control and Complications Trial/Epidemiology of Diabetes Interventions and Complications (DCCT/EDIC) Study.

A graphical overview is given in Supplemental Figure 4.

CKDGen Stage 1 Discovery Meta-analysis

In the stage 1 (discovery) meta-analysis we searched for SNPs associated with UACR or MA in 12 CKDGen population-based cohorts totaling $n = 31,580$ patients of European descent. Individual GWA analyses encompassing approximately 2.5 million imputed SNPs were performed within each of the 12 stage 1 (discovery) CKDGen population-based cohorts. In each cohort, these analyses were performed in the overall group and separately in patients without diabetes. Next, we conducted four meta-analyses combining the study-specific UACR or MA GWA analysis results (i) including all patients and (ii) separately in patients without diabetes. From these four sets of meta-analysis results, we selected a list of independent SNPs (pairwise $r^2 < 0.2$) with a P value $< 1 \times 10^{-6}$ and minor allele frequencies (MAF) $> 5\%$. The 16 highest ranking SNPs from this list were then selected for CKDGen stage 2 follow-up to replicate our findings.

CKDGen Stage 2 Follow-up Meta-analysis

Association testing for each of the 16 SNPs for UACR and MA was performed in each of the 15 independent CKDGen stage 2 cohorts totaling $n = 27,746$ individuals of European descent, again, including all patients and separately in patients without diabetes. Study-specific association results of the 16 SNPs were then meta-analyzed across stage 2 studies.

SNPs showing evidence of replication in CKDGen stage 2 were further evaluated for their effects both in the presence and absence of diabetes and hypertension as major risk factors of albuminuria.

CARE Discovery Association Analysis

The CARE Consortium consists of nine studies. For the present analysis, we included five studies in European Americans (19,499 patients in total) and five studies in African Americans (6981 patients in total) with the IBC SNP chip.¹⁴ Study-specific genetic association analysis of UACR and MA were performed in the same manner as in CKDGen. CARE study-specific results were then meta-analyzed within each ethnic group for both UACR and MA.

Joint CKDGen and CARE Meta-analysis

For SNPs that reached genome-wide significance in the combined CKDGen stage 1 and stage 2 meta-analysis and were also significant in the CARE meta-analysis, we conducted meta-analyses for UACR and MA across a total of 28 nonoverlapping cohorts: in 9 CKDGen stage 1 studies with 16,667 patients (excluding ARIC, CHS, and FHS since they were also members of the CARE Consortium), 14 CKDGen stage 2 follow-up studies with 26,987 patients (excluding ARIC in silico results), and 5 CARE European American cohorts with 19,499 patients, involving a total of 63,153 patients of European descent.

Follow-up Analysis in DCCT/EDIC

Significant SNPs from the joint CKGen and CARE meta-analysis were replicated in the DCCT/EDIC Study, which currently consists of 1304 Caucasian participants who underwent genotyping on the

Illumina 1M SNP chip. This is a longitudinal study using Cox proportional hazards models to analyze time to renal events (see definition of the outcome below).

Study-Specific Information and Statistical Analysis

In all studies, all participants gave informed consent. All studies were approved by their appropriate Research Ethics Committees.

A list of all contributing studies is given in [Table 1](#) and more study-specific information including genotyping and imputation methods are given in Supplemental Table 1, A and B, as well as in the Study-Specific Methods Section of the Supplemental material. Details on statistical analyses on the study-specific level as well as for meta-analyses are given in the Supplemental material.

Outcomes and Covariates

In each of the CKDGen and CARE studies, the continuous outcome urinary albumin-to-creatinine ratio (mg/g, measured as described in the Study-Specific Methods section in the Supplemental material) as well as the dichotomous outcome microalbuminuria (MA, defined as urinary albumin-to-creatinine ratio >17 mg/g for men and >25 mg/g for women^{40,41}) were analyzed. For creating the continuous trait UACR used in the analysis, urinary albumin-to-creatinine ratio was log-transformed, and sex-specific residuals were computed by regression on age and, in multicenter studies, on study center.

Hypertension was defined as systolic BP ≥ 140 mmHg, diastolic BP ≥ 90 mmHg, or treatment; and diabetes was defined as fasting plasma glucose of at least 126 mg/dl or treatment if not stated otherwise in the study-specific methods. We estimated GFR (eGFR) using the four-variable MDRD formula as described previously¹⁸ to determine the prevalence of chronic kidney disease (defined as eGFR <60 ml/min per 1.73 m²) in each cohort.

In DCCT/EDIC, renal outcomes were (1) time from DCCT baseline until persistent microalbuminuria, defined as time to two consecutive albumin excretion rates (AERs) >30 mg/24 h (>20.8 μ g/min), and (2) severe nephropathy, defined as the time to AER >300 mg/24 h (>208 μ g/min) with prior persistent microalbuminuria or end-stage renal disease).

Genotypes

All the studies in CKDGen stage 1 had genotype data from genome-wide SNP arrays available, whereas the studies in the CARE Discovery studies genotyped the IBC SNP array,¹⁴ a gene-centric array containing 50,000 SNPs tagging genes across a range of cardiovascular, metabolic, and inflammatory syndromes. In CKDGen, the genotyped SNPs were imputed to approximately 2.5 million HapMap SNPs based on HAPMAP CEU samples. Imputation provides a common SNP panel across all studies to facilitate a meta-analysis across all contributing SNPs. Information on study-specific genotyping platforms and imputation procedures are presented in Supplemental Table 1, A and B. Information on genotyping in CKDGen stage 2 cohorts are given in the Study-Specific Methods section of the Supplemental material.

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Supplementary Material

Supplemental Data:

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Author contributions:

Study design: E.I., J.A., S.K., R.R., K.E., S.S., H.V., N.J.W., P.P.P., B.P., F.K., Y.L., T.B.H., C.H., O.D., O.P., H.C., I.R., V.V., P.V., G.W., V.M., D.W., E.B., J.C., W.H.L.K., A.K., A.P., I.H.D., N.L.G., M.G.S., L.F., C.A.B., M.O., T.I., H.E.W., I.M.H., M.S., A.T., P.K., C.S.F., L.L., T.B.H., V.G., E.I., J.A., A.D.P., S.B.B., DCCT/EDIC.

Study management: E.I., J.A., S.K., S.T., R.R., K.E., R.B., H.V., R.F.J.L., N.J.W., C.P., C.F., P.P.P., B.K., L.K., B.P., F.K., S.C., Y.L., T.B.H., O.P., H.C., I.R., P.V., G.W., V.M., D.W., E.B., J.C., W.H.L.K., A.P., B.D.M., A.R.S., T.T., C.A.B., M.O., T.I., J.B., H.E.W., W.K., B.K.K., I.M.H., A.Tö., C.S.F., G.E., L.L., T.B.H., V.G., E.I., J.A., K.A., A.D.P., DCCT/EDIC, G.N., P.V.D.H., S.J.L.B.

Patient recruitment: J.A., S.T., R.R., R.B., S.S., H.V., N.J.W., P.P.P., B.P., T.B.H., O.P., I.R., P.V., G.W., J.C., B.D.M., A.R.S., T.I., H.E.W., A.T., C.S.F., G.E., V.G., G.C., J.A., S.H., K.A., DCCT/EDIC, N.H., S.J.L.B., G.N., E.I., J.A., A.S.

Interpretation of results: E.I., J.A., S.K., M.A., S.T., E.A., R.R., K.E., A.T., H.K.K., R.B., S.S., H.V., C.P., C.F., C.M., P.P.P., B.K., B.P., F.K., S.C., Y.L., T.S.L., T.B.H., C.H., O.D., V.V., J.B., M.B., J.C., W.H.L.K., A.K., A.P., I.H.D., N.L.G., M.G.S., J.E., C.A.B., M.O., W.K., B.K.K., P.V.D.H., S.J.L.B., G.N., I.M.H., C.S.F., L.A.C., C.-T.L., A.D., E.I., J.A., A.D.P., S.B.B., DCCT/EDIC, A.D.J.

Manuscript writing: S.K., R.R., C.P., J.B., M.B., W.H.L.K., A.K., A.P., I.H.D., C.A.B., M.O., I.M.H., C.S.F., C.O.S., J.B.M., L.A.C., C.-T.L., A.D., A.T., M.H.C.

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Statistical methods and analysis: E.I., M.A., E.A., A.Te., J.L., J.Z., C.P., C.F., B.K., F.K., S.C., Y.L., K.L., C.H., V.V., Z.K., S.B., D.E.K., M.L., A.K., J.O., N.L.G., T.L., T.T., J.E., C.A.B., M.O., I.M.H., I.P., C.S.F., J.H., A.V.S., T.A., V.G., L.A.C., C.-T.L., X.L., E.A., A.Ti., E.I., J.A., R.M., A.D.P., S.B.B., P.V.D.H., G.N., S.J.L.B., DCCT/EDIC, M.H.C.

Genotyping: A.C.S., M.A., A.Ti., H.K.K., R.F.J.L., N.J.W., F.K., S.D., Y.L., C.H., V.V., E.B., T.H., D.H., C.A.B., T.I., H.E.W., P.K., G.C., A.C.S., J.I.R., S.H., F.S., A.D.P., S.C., E.I., J.A., A.S., P.V.D.H., A.Te., A.Ti.

Bio-informatics: E.I., A.D.J., H.K.K., J.L., J.Z., C.F., K.L., C.H., V.V., Z.K., S.B., E.B., J.O., N.L.G., C.A.B., M.O., I.M.H., I.P., S.J.H., Q.Y., A.V.S., T.A., E.I., J.G.M., M.H.C., P.V.D.H., A.Te., A.Ti.

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Members of the CKDGen Consortium: Anna Köttgen, Cristian Pattaro, Carsten A. Böger, Christian Fuchsberger, Matthias Olden, Nicole L. Glazer, Afshin Parsa, Xiaoyi Gao, Qiong Yang, Albert V. Smith, Jeffrey R. O'Connell, Man Li, Helena Schmidt, Toshiko Tanaka, Aaron Isaacs, Shamika Ketkar, Shih-Jen Hwang, Andrew D. Johnson, Abbas Dehghan, Alexander Teumer, Guillaume Paré, Thor Aspelund, Gudny Eiriksdottir, Lenore J. Launer, Tamara B. Harris, Evadnie Rampsaud, Braxton D. Mitchell, Eric Boerwinkle, Maksim Struchalin, Margherita Cavalieri, Andrew Singleton, Francesco Giallauria,

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Figures and Tables

Table 1.
Study sample characteristics in the CKDGen and CARE Consortia

Study	n ^a	Women %	Age, years	UACR ^b	MA %	CKD %	HTN %	DM %
Stage 1: GWAS								
Amish	744	45.0	42.8	3.8 (2.2, 6.1)	NA	1.2	11.6	0.7
ARIC	6525	53.1	63.1	3.9 (2.0, 7.7)	9.4	9.1	42.9	13.6
BLSA	354	46.9	69.8	7 (4.4, 11.0)	NA	15.5	53.7	14.4
CHS	1865	60.8	71.2	9.3 (5.3, 19.9)	23.0	16.0	61.2	13.7
Colaus	5311	53.2	53.4	5.1 (3.4, 9.1)	9.5	3.8	36.1	9.6
EPIC	2371	53.3	59.2	3.6 (1.5, 8.3)	8.1	NA	49.3	3.0
Fenland	1398	56.2	44.9	4.5 (3.2, 7.1)	5.5	0.9	18.9	1.4
Framingham Heart Study	6523	53.2	47.6	4.6 (2.6, 9.9)	9.6	3.4	27.4	5.3
KORA F3	1530	50.5	62.5	4.9 (2.1, 11.1)	11.7	10.8	41.1	10.3
KORA F4	1803	51.3	60.9	10.7 (7.0, 18.4)	20.9	7.0	20.9	9.2
Micros	503	56.3	46.0	NA	5.4	3.6	40.6	3.7
SHIP	2653	48.9	55.3	8.9 (5.0, 20.6)	25.3	8.5	54.2	12.4
Stage 2								
AGES	3196	57.9	76.4	2.66 (1.2, 7.0)	11.9	24.2	80.6	11.6
Amish	695	54.4	47.2	7 (4.3, 13.5)	NA	NA	21.0	11.5
ARIC	759	56.0	63.0	3.9 (2.1, 7.5)	7.6	7.7	39.3	13.1
GENOA	987	43.0	59.0	3.1 (1.7, 5.9)	6.4	10.7	73.5	15.8
Health ABC	211	27.0	73.9	13.9 (6.1, 49.6)	42.2	25.0	64.1	100.0
HUNT	2386	54.5	51.4	6.1 (4.4, 9.2)	8.6	4.7	43.4	4.0
KORA F3	1392	52.4	50.8	4.4 (1.9, 9.6)	10.9	5.5	28.6	4.5
KORA F4	1197	52.3	49.2	10.1 (6.6, 20.1)	23.7	5.9	13.4	4.0
KORCULA	863	63.9	56.3	4.6 (2.5, 10.4)	12.4	7.5	57.3	10.4
Nurses Health Study	4138	100.0	58.2	2.8 (1.7, 4.5)	3.6	10.4	36.1	4.4
PREVEND	7803	50.5	49.5	7.1 (4.8, 13.3)	16.7	6.4	33.5	3.7

SAPHIR Study	1707	37.3	51.4	3.8 (2.3, 8.2)	9.8	1.4	56.5	3.2
SORBS	877	58.7	48.0	6.8 (4.6, 13.5)	13.6	4.0	52.1	9.2
SPLIT	472	56.5	49.3	2.5 (1.3, 5.8)	7.8	3.6	39.4	5.1
ULSAM	1063	0.0	71.0	7.5 (4.9, 16.1)	15.9	15.2	74.0	11.0
CARE Consortium								
European Americans ^c								
CARDIA	1242	50.4	40.7	4.4 (3.3, 6.9)	4.5	0.53	9.3	5.0
MESA	2289	52.1	62.7	4.7 (3.1, 8.6)	9.6	9.7	38.7	6.3
African Americans								
ARIC	2256	64.5	61.7	2.7 (0.9, 9.6)	16.3	7.3	70.9	27.7
CARDIA	1089	56.3	39.5	4.3 (3.1, 7.4)	9.6	0.9	24.7	6.4
CHS	426	64.3	72.1	10.9 (5.0, 26.9)	31.9	18.4	68.2	24.4
Jackson Heart Study	1530	58.5	51.8	6 (4.0, 13.0)	17.8	5.9	58.8	16.1
MESA	1680	54.6	62.2	5.5 (3.1, 13.2)	16.6	8.5	59.8	17.8

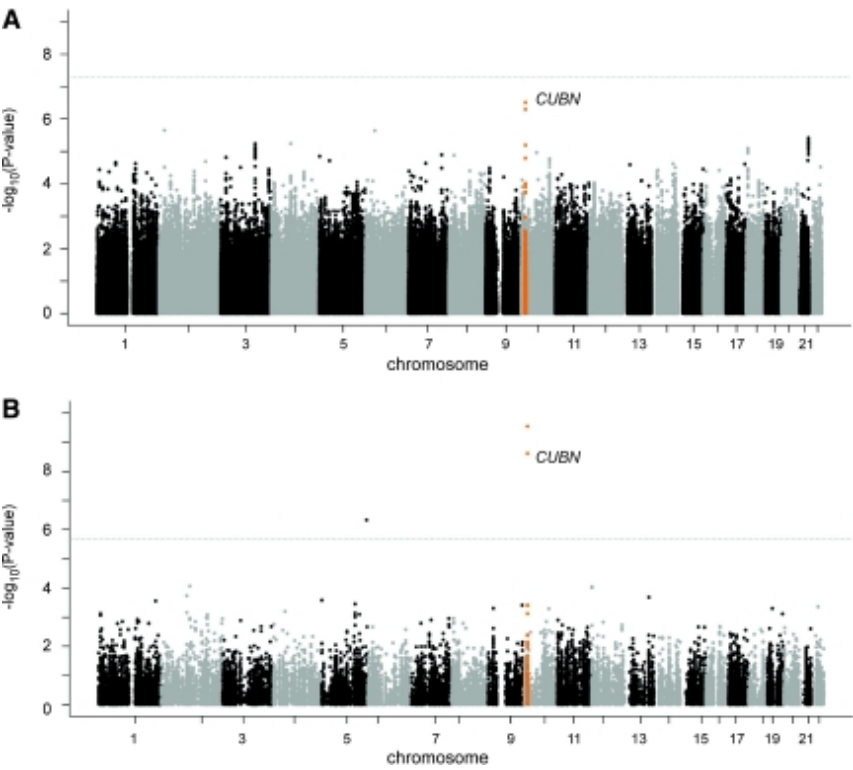
Data presented as means except where otherwise indicated. DM, diabetes; HTN, hypertension.

^aRefers to the successfully genotyped and analyzed sample with UACR or MA data, which may differ from the recruited sample described in Supplemental online Methods.

^bMedian (interquartile range: 25th percentile, 75th percentile).

^cRefers to studies that are nonoverlapping with CKDGen; the sample size of ARIC, CHS, and FHS in CARE was 7687, 2073, and 6208, respectively.

Figure 1.



Genome-wide log₁₀ *P* value plot from stage 1 analyses of UACR. Participants of European ancestry in the CKDGen Consortium (A) and the CARE Consortium [IBC chip analyses; (B)].

Table 2.

Results for CUBN SNP rs1801239 on chromosome 10 in the CKDGen and CARE Consortia^a and DCCT/EDIC

	UACR <i>P</i> Value ^b	Microalbuminuria <i>P</i> value ^c	Odds Ratio (95% CI) for Clinical Outcomes per Copy of Minor C Allele
Overall samples			Microalbuminuria (MA)
CKDGen Stage 1 discovery	3.0 × 10 ⁻⁷	8.7 × 10 ⁻⁷	1.25 (1.15 to 1.37)
CARE IBC discovery in European Americans	2.9 × 10 ⁻¹⁰	2.4 × 10 ⁻⁷	1.31 (1.18 to 1.45)
CKDGen Stage 2 follow-up	0.02	0.43	1.01 (0.98 to 1.05)
Combined populations of European ancestry ^d	1.1 × 10 ⁻¹¹	0.001	1.06 (1.02 to 1.09)
CARE African Americans	0.005	0.008	1.42 (1.10 to 1.84)
Diabetes stratified ^d			
no diabetes	3.2 × 10 ⁻⁸	0.06	1.03 (1.00 to 1.07)
diabetes	0.006	4.7 × 10 ⁻⁴	1.27 (1.11 to 1.45)
Hypertension stratified ^e			
no hypertension	1.3 × 10 ⁻⁶	6.0 × 10 ⁻⁴	1.23 (1.09 to 1.38)
hypertension	7.5 × 10 ⁻⁸	1.4 × 10 ⁻⁷	1.34 (1.20 to 1.49)
DCCT/EDIC ^f			
			Persistent MA
simple model		0.02	1.42 (1.08 to 1.88)
extended model		0.02	1.41 (1.06 to 1.87)
			Severe Nephropathy
simple model		0.53	1.14 (0.76 to 1.69)
extended model		0.67	1.10 (0.72 to 1.67)

^aSample sizes are as follows (microalbuminuria case numbers in parentheses): CKDGen Stage 1: 31580 (3698); CARE European Americans: 19,499 (2100); CKDGen Stage 2: 27,746 (3313); CARE African Americans: 6981 (1159).

^b*P* values from CKDGen and CARE European and African American Stage 1 analyses are from the inverse variance weighted fixed effects method, and *P* values from the CKDGen Stage 2 analyses, the combined analyses, and the hypertension- and diabetes-stratified analyses are from the sample size weighted Z score method. In all analyses, the minor allele C showed an increase in UACR, direction consistent with the odds ratio for MA.

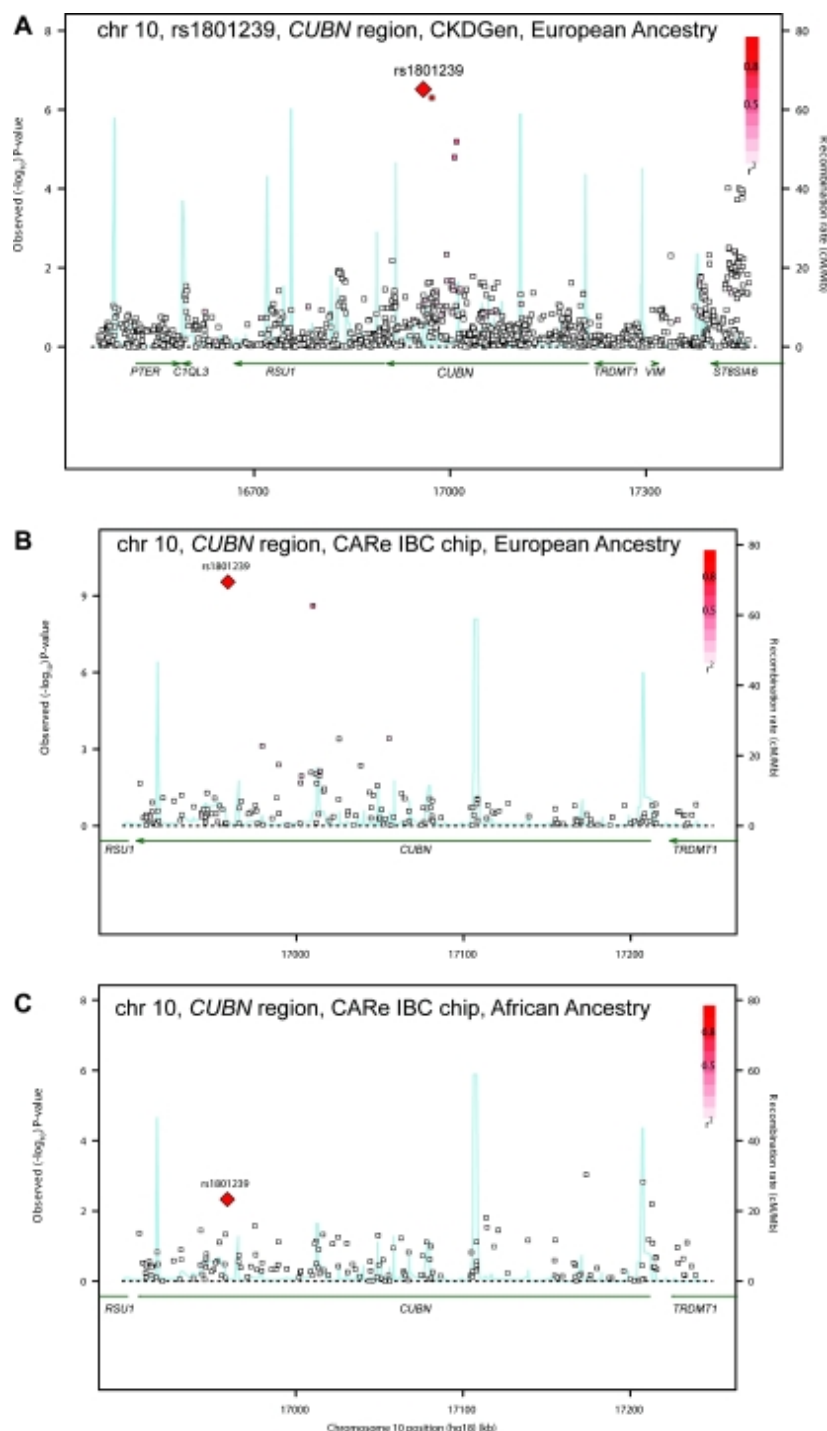
^c*P* values from inverse variance weighted fixed effects model.

^dCombined populations of European ancestry, includes CKDGen Stages 1 and 2 (after removal of ARIC, CHS, and FHS) and all five cohorts of CARE European Americans: 63,153 (7383 microalbuminuria cases).

^eCombined populations of European ancestry, includes CKDGen Stage 1 (after removal of ARIC, CHS, and FHS) and all five cohorts of CARE European Americans: 36,166 (4128 microalbuminuria cases).

^fModeled as hazard ratio; $n = 1304$ including 318 cases of persistent microalbuminuria and 116 cases of severe nephropathy.

Figure 2.



Regional Association Plot for the *CUBN* gene region. CKDGen Consortium stage 1 analyses (A), CARE IBC SNP chip results in participants of European Ancestry (B) and African ancestry (C). $\log_{10} P$ values are plotted versus genomic position (build 36). The lead SNP in each region is labeled. Other SNPs in each region are color-coded based on their LD to the lead SNP (LD based on the HapMap CEU and YRI for the participants of African ancestry; see color legend). Gene

annotations are based on UCSC Genome Browser (RefSeq Genes, b36) and arrows indicate direction of transcription. Graphs were generated using the software SNAP (<http://www.broadinstitute.org/mpg/snap/index.php>). Regions vary between panels because there was no coverage beyond the *CUBN* gene on the IBC chip used to generate panels B and C.

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